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Newsletter for the USDA Plant Genome Research Program

Volume 4, No. 3/4 August 1994-January1995

USDA Plant Genome Research Program Progress Report

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The Plant Genome Research Program (PGRP) addresses agricultural problems. Solution of the problems will lead to efficient production of food, feed, and fiber. While concurrently reducing the environmental impact associated with farming practices and manufacturing processes.

The goal of the program has remained the same for the past four years. It was established to speed the improvement of plants - agronomic, horticultural, and forest tree species. This is accomplished by locating and characterizing agriculturally important genes and by subsequent transfer of those genes to plants to improve performance. The products, through the hands of the breeder, will be new cultivars. These new cultivars will offer pest and disease resistance and tolerance to abiotic stresses, such as heat, drought, and cold. They will meet future marketplace needs and niches, as well as strengthen endeavors to enhance the environment.

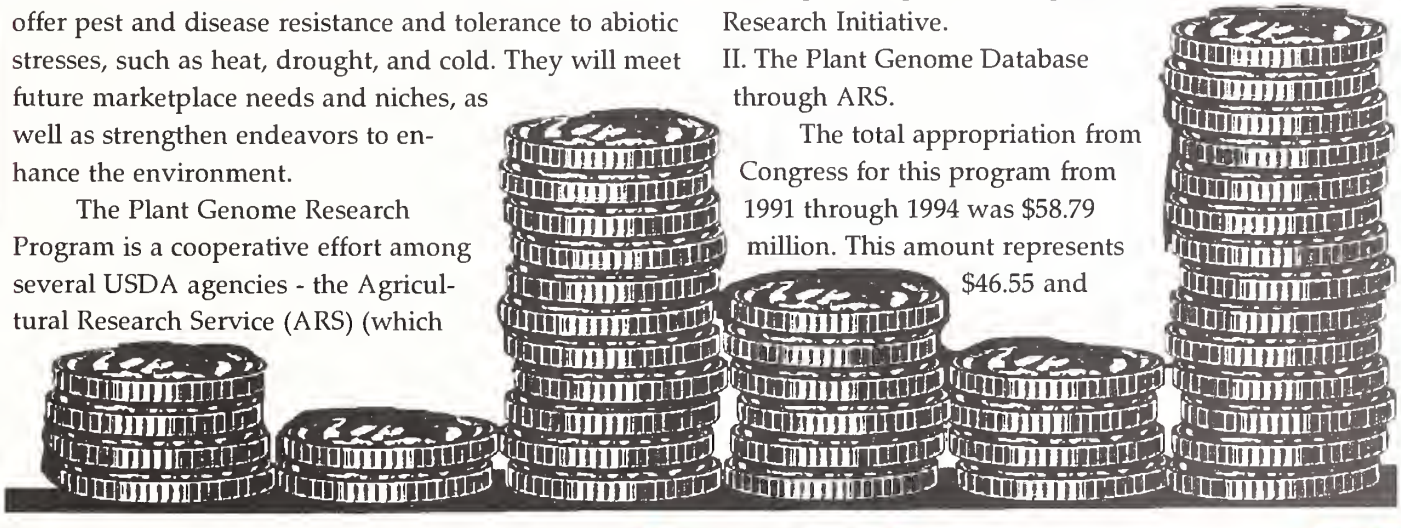
The Plant Genome Research Program is a cooperative effort among several USDA agencies - the Agricultural Research Service (ARS) (which now includes the National Agricultural Library (NAL)) is the lead agency, and the Cooperative State Research, Education, and Extension Service (CSREES). ARS coordinates with the Human Genome Projects of the National Institutes of Health (NIH) and the Department of Energy (DOE), as well as the *Arabidopsis thaliana* effort of the National Science Foundation (NSF). The Plant Genome Research Program is in the process of establishing official cooperation with some of the European Union (EU) countries and informal but promising interactions with several Pacific Rim countries.

The USDA Plant Genome Research Program is a single program with two components:

I. Competitive grants through CSREES, National Research Initiative.

II. The Plant Genome Database through ARS.

The total appropriation from Congress for this program from 1991 through 1994 was $58.79 million. This amount represents $46.55 and



$12.24 million dollars designated for the National Research Initiative competitive grants and the Agricultural Research Service, respectively.

I. COMPETITIVE GRANTS NRI COMPONENT

Grant proposals are oriented towards improving agronomic qualities through genomic research. The Request For Proposals (RFP) address three categories: 1. Broad genome maps; 2. Fine maps, including physical mapping; and 3. Technology development to increase the efficiency of mapping and sequencing desirable genes.

Competitive grants were awarded to 381 scientists from 84 public, private and government research institutions from 43 states (Table 1). The average award per year over the four years was $127,177 with an average rate of success of 32.8% and an average of 2.2 years per award (Table 2). Fifty-one agronomic, horticultural, and forest tree species and three non-agricultural taxa are included in the plant genome effort (Table 3). Eighty four percent of the grant funding went to members of five plant groups: 1. Tree species - $1.8 million; 2. Crucifers - $4.3 million; 3. Legumes - $5.9 million; and grasses - $16.6 million. Nearly 100 gene/trait/genetic phenomena are at various stages of progress as listed in Table 4. Table 5 lists some of the molecular biology technology pursued by awardees of the grant program over the past four years.

Several important accomplishments have been made by the Program grant awardees:

- For the first time ever, a disease resistance gene was isolated by map-based cloning technology. The bacterial speck resistance gene was molecularly transferred to a susceptible variety, resulting in resistance.
- One awardee is part of a team that discovered a new class of genes that allows a plant to recognize a diverse group of pathogens.
- Quantitative trait loci (QTL) methods have been used to develop a barley line resistant to barley stripe rust which increased the yield of corn by 15%.
- Researchers have analyzed the loblolly pine genome and mapped over 200 genetic markers as part of a tree improvement program in the Southeastern United States. Tree breeders can now expedite the improvement of loblolly pines by shortening the time necessary to select desirable characteristics and by using these genetic markers to identify trees with desirable traits.

The above achievements represent only a small fraction of the program's effort. Development of molecular genomic maps for corn, wheat, sorghum, soybean, cotton, tomato, peanut, lettuce, apple, and other commodities is progressing rapidly and the association of the markers with desirable genetic traits will facilitate plant breeding and crop improvement efforts. This activity of placing the DNA gene locations in the hands of the breeder is a paramount goal of the USDA Plant Genome Research Program.

II. PLANT GENOME DATABASE COMPONENT

With the aid of molecular geneticists and breeders, the PGRP is achieving its aims by locating and

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Table 1

Institutions Receiving NRI Plant Genome Awards 1991-94

Alabama	Idaho	Oregon
Arizona	Illinois	Oregon State
Auburn	Illinois State	Penn State
Bethesda	Indiana	Purdue
Boston U	Iowa	Rhode Island
Botanical Society	Iowa State	Rutgers
Boyce Thompson	Kansas State	Salk Institute
Brandeis	Kentucky	Scripps
Cal Berkeley	Maine	Southern Miss
Cal Davis	Maryland	Tennessee
Cal Irvine	Mass Gen Hospital	Texas
Cal Riverside	Mass Inst Tech	Texas A&M
Cal San Diego	Michigan State	Texas Tech
Case Western	Minnesota	U Detroit Mercy
Clemson	Mississippi State	UCLA
Cold Spring Harbor	Missouri	USDA Forest
Colorado	Montana State	USDA/ARS
Colorado State	N Arizona	Utah
Cornell	Nebraska	Utah State
DNA Plant Tech	Nevada Las Vegas	Virginia Tech
Drexel	New Hamphire	Wash U St Louis
Duquesne	New Mexico State	Washington
Federation of Biology	New York	Washington State
Florida	New York State	Wellesley College
Florida A&M	North Carolina	Wells College
Florida State	North Carolina State	Wisconsin
Georgia	North Dakota	Yale
Harvard	North Dakota State	
Hawaii	Ohio State	

using genes that improve plants. The program uses the intellectual prowess of government, university, and private sector researchers.

Collaboration of many researchers throughout the country and the world necessitates the need for electronic media communication. Plant genome research generates voluminous data and the handling of large amounts of information requires researchers to have computer expertise.

Performing experiments in the laboratory or field and publishing results in regular scientific journals will not adequately meet the information demands of the 21st century. The ability to rapidly assimilate, analyze, and compare research findings in an electronic form will be needed.

Voluminous data generation requires a Plant Genome Database (PGD). It is divided into three components:

1. Stock Center Databases - These databases consist of data necessary to

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National Agricultural Library

Table 2

NRI PLANT GENOME REVIEWED AWARDS 1991-94

Year	Awards	$Amount	Avg Years Per Award	Average $ Per Award	% Success Rate
1991	76	10,489,525	2.2	138,020	30
1992	95	12,191,822	2.1	128,335	34
1993	91	12,126,238	2.3	133,255	34
1994	104	11,730,074	2.0	112,876	33
Totals/Avg	366	46,546,659	2.2	127,177	32.8

*Total dollars, not per year

enhance genomic research. They are located throughout the United States and elsewhere and are of utmost importance to the USDA PGD and plant breeders in general to making the desired genetic variation available to address agricultural problems. At present, there is a database called GRIN, Germplasm Research Information Network, and while not a direct part of the plant genome research program, it provides a valuable link between germplasm and the genetic information from the other databases (See article on page 21).

2. Genome Mapping Database - includes physical, genetic, RAPDs, RFLPs, and other map types of many agricultural plant species and some model systems from non-agricultural taxa. These databases are being developed for the first time in a coordinated manner under the direction of the program. At present, ARS is funding directly and indirectly the databases for *Arabidopsis thaliana* and *Chlamydomonas* species (model systems), apple, barley, beans, corn, cotton, oats, peas, pepper, petunia, pine, poplar, potato, rye, sorghum, sugarcane, tobacco, tomato, Triticum species -- and the list is expanding.

3. DNA Sequences - Since this data is the same as those which are being placed into GenBank/GenInfo/European Molecular Biology Laboratories (EMBL) and DNA Databank of Japan (DDBJ), it was the consensus not to have a separate independent sequence database. Hence, all plant DNA sequence data from the USDA Plant Genome Research Program are being placed in the above sequence database efforts of the Plant Genome Database program.

The Agricultural Research Service is concerned only with mapping databases through a rather simple but efficient process. Funding, direct and indirect, is supplied by ARS to "database curators" for the various species. These researchers take the lead for their respective species, perform some evaluation and quality control of their databases, and hold that information in the home laboratories of their institution. The information is sent to the USDA National Agricultural Library, where it is integrated into a master or central database system with data from all of the species. The priority database topics include disease/pathology, genetic resources,

Table 3

Species Represented by Plant Genome Awards

Agrobacterium	*Cyanophyta*	Poplar
Alfalfa	Douglas fir	Prunus
Apple	Eucalyptus	Rice
Arabidopsis	Flax	Rye
Asparagus	Grape	Sesbania
Barley	Legumes	Sorghum
Bean	Lettuce	Soybean
Blueberry	Maize	Spinach
Brassica	Mungbean	Strawberry
Cabbage	Oats	Sugarcane
Carrot	Onion	Sunflower
Chlamydomonas	Pea	Sweet potato
Chysanthemum	Peach	Sweetclover
Citrus	Peanut	Tobacco
Cotton	Pepper	Tomato
Cucumber	Petunia	Wheat
Cuphea	Pine	Wild rice

Table 4

Genetic Phenomena NRI Plant Genome Awards 1991-94

Abscission enzyme synthesis
Abscission zone formation
Acylsugar biosynthesis
Agrobacterium mediated transformation
Amylase activation & repression
Annual growth rate
Anthocyanin biosynthesis
Apomixis, asexual reproduction
Blue-light signal transcription
Cell growth
Centromere organization
Chromosome recombination
Chromosome sorting libraries
Cloning disease resistance genes
Cold resistance
Cytokinin mRNA regulation
Cytokinin response
Developmental regulation
Disease resistance
Drought tolerance
Endodormancy & chilling requirement
Ethylene biosynthesis
Fertility restoration/CMS cytoplasm
Flower sex determination
Fruit/flower development
Gametophytic lethal screening
Gene effects on chromatin structure
Gene tagging for insect resistance
Genetic engineered sterility
Gene/chromosome identification
Gibberellin synthesis
Growth rate
Homologous recombination
Homozygous deletion stocks
Hormonal control of seed maturation
Hormonal rRNA transcription
Hypersensitive disease response
In situ hybridization
Infloresence development, flowering
Lipid desaturation
Maysin synthesis
Metabolic transport
Microsatellite sequences
Mitochondrial DNA replication
Mitochondrial sequencing
mRNA stability in dicots
Mutation via transposable elements
Nematode resistance
Nodulation & N fixation
Nuclear targeting of DNA
Nuclear & organelle DNA variation
Nuclear-plastid communication
Nucleolar dominance
Oxidase expression
Photorespiration, nitrogen assimilation
Photosynthesis
Phytoalexin enzyme induction
Phytochrome A, mRNA degradation
Phytochrome gene control
Plant transformation/YACs
Plasmid directed conjugation
Polyadenylation
Position effects
Proline degradation
Purine metabolism
Pyramiding resistance genes
Repeat induced gene silencing
RNA editing
Root Nodule morphogenesis
Seed oil synthesis
Self incompatibility
Sequence repeats, microsatellites
Signal transduction
Simple sequence repeats
Site directed mutagenesis
Somatic mutation
Spatial organization of genome
Starch metabolism & transport
Tandem repeat sequences
Targeted DNA integration
Thylakoid membrane biogenesis
Transformation disease resistance
Transformation drought tolerance
Transformation insect resistance
Transformation virus resistance
Translation control
Transposable elements
Transposon tagging
Triacylglycerol biosynthesis
T-DNA transfer, and transport
Ubiquitin activating enzymes
Winter hardiness
Wound inducible insect resistance
YAC size DNA

Table 5

Examples of Technology Development NRI Plant Genome Grants 1991-94

Antibody synthesis for proline
Biolistic transformation with high molecular weight DNA
Characterize cytokinin induced mRNA stability
Characterize Ubiquitin regulation
Chromosome painting
Construction and insertion of chimeric gene
Construction of directed transpositions
Detection of microsatellite loci
Develop system for import of nucleic acid
Develop vectors for plant YAC transformation
Develop target probes for fly resistance
DNA vector synthesis
Functional cloning of disease resistant genes
Identification of effective sterility genes
In situ hybridization
Isolate nuclear skeletal structures
Map based cloning system
Map polymorphic simple sequence repeats
Megabase DNA isolation
Molecular marker assisted screening
Molecular probe and reagent development
Post transcriptional control
Regeneration after transformation for Pine
Site directed mutagenesis
Site-selected insertion
Statistical methods to map QTLs
Substrate features required for enzyme activation
Transfer teosinte chromosomes to maize
Transformation system for Peanut
Transposon tagging
Wound induced transformation

germplasm, genetic maps, metabolic pathways, organelle maps, quantitative traits and other factors as decided upon by the database operators. Links are made to relevant databases such as GenBank/EMBL/DDJB, SwissProt, and Agricola.

All of the information in the database is accessible to the public. The Plant Genome Database is now a real and functioning information and data resource for agricultural genome researchers. As the system increases in size and intellectual content, its value will greatly increase and enhance the abilities of researchers to undertake more sophisticated genome research, which will ultimately benefit the agricultural community and all consumers. ◆

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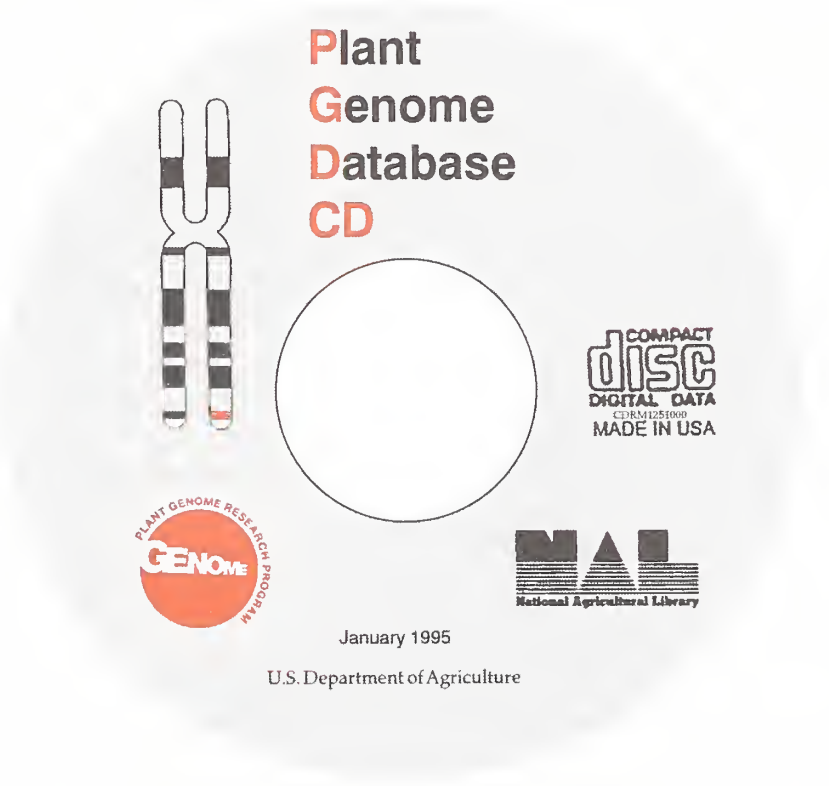


Check the appropriate box on the last page of this newsletter and mail it back to us with a self-addressed label. The Plant Genome Data and Information Center will gladly mail you a free CD.

THERE IS A NEW RELEASE OF THE PLANT GENOME DATABASE ON CD. *FREE OF CHARGE.*

Off the Wire

Internet Computer Index Centralizes Information About Computers

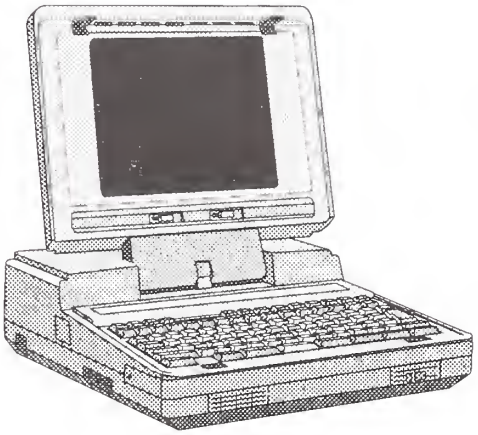
Free service gives easy access to widely dispersed Internet resources

Santa Cruz, California- Dec. 12, 1994 - For the first time, Internet users can find almost any computer-related information on the Internet in one central location. The Internet Computer Index (ICI), created by Proper Publishing, leads users to the best information available on the Internet relating to PCs, Macintoshes, and Unix computers. Additional information is available on ICI that cannot be found anywhere else on the Internet.

ICI uses the World Wide Web and Gopher systems to distribute its information. Using menus and hypertext, ICI gives up-to-date connections and pointers to freely available information on the Internet. Anyone on the Internet, anywhere in the world, can access ICI 24 hours a day at no charge.

Description of ICI

ICI is the Internet's only one-stop, resource-locating service. Users can find answers to their hardware and software questions, solve networking problems, research buying decisions, and keep up to date with their systems. ICI contains pointers to all Usenet news groups, mailing lists, Gopher and World Wide Web servers, anonymous FTP sites, and



other Internet-specific resources.

In order to simplify searching, ICI is organized in hierarchical menus of information. For each type of computer system (PC, Macintosh, or Unix), a menu lists the Internet resources within that system. Users also can traverse among the three menus by way of cross-links.

Internet resources in ICI include the following:

- Usenet news groups
- mailing lists
- Gopher servers
- World Wide Web servers
- anonymous FTP sites
- frequently asked questions files (FAQs)
- online publications
- commonly downloaded files

Accessing ICI

To reach ICI using a Gopher program, enter "ici.proper.com" as the host name. For American Online users, ICI is found in the Gopher area in the "Computers" folder.

To reach ICI using a World Wide Web program such as Mosaic, enter "http://ici.proper.com" as the Universal Resource Locator (URL).

Public contact: Send e-mail to info@proper.com ◆

Mention of a trade name or brand does not constitute endorsement or recommendation by the Department over similiar products not named.

Touching Base with Martin Sachs

The Maize Genetics Cooperation * Stock Center

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The Maize Genetics Cooperation originated at an evening get-together in R.A. Emerson's hotel room during the 1928 Genetics Society of America meeting. During that meeting a dozen or so maize workers discussed the current state of maize linkage maps.

The formal organization of the Maize Genetics Cooperation occurred in August 1932, when maize geneticists attending the 6th International Genetics Congress agreed to establish a cooperative enterprise to further the advance of maize genetics. Among the aims of this organization was the collection and dissemination of unpublished maize data and information to interested workers and the maintenance and distribution of tester stocks (Rhoades, 1984).

The establishment of the Maize Genetics Cooperation promoted the sharing of genetic marker stocks that have been developed by maize geneticists over the years in a spirit of cooperation and generosity. Marcus M. Rhoades was asked to serve as custodian of the Maize Genetics Cooperation and was therefore the first secretary of the Maize Genetics Cooperation * Newsletter (present secretary is Ed Coe, USDA/ARS & University of Missouri-Columbia) and the first director of the Maize Genetics Cooperation * Stock Center.

In 1953, Marcus Rhoades and Earl Patterson moved the collection of maize stocks from Cornell University to the University of Illinois in Urbana. The Maize Genetics Cooperation * Stock Center has been a major part of the University of Illinois Department of Agronomy since then, being directed by faculty members Bob Lambert (16 years) and Earl Patterson (20 years).

Over the past 15 years, USDA/ARS began playing an increasingly active role in supporting the operations of the Stock Center. While the Maize Genetics Cooperation * Stock Center continues to be housed in the UI Department of Agronomy, in 1992 ARS took over the day-to-day operations of the Stock Center and an ARS scientist was appointed as Director. In 1993, an ARS support scientist was appointed to serve as Curator.

Presently, Marty Sachs serves as Director, Philip Stinard serves as Curator and Janet Day serves the Stock Center as a Research Specialist with the University of Illinois Department of Agronomy. Earl Patterson, who retired in 1993, continues to be active in serving the Stock Center.

The Maize Genetics Cooperation * Stock Center is now the main repository for maize mutants utilized in research by cooperators worldwide. It is an essential resource to maize scientists conducting basic and applied biological research. It is the goal of the Maize Genetics Cooperation * Stock Center to acquire, maintain and make available stocks containing all known allelic and

cytological variation in maize and information about them. Information about maize mutants and chromosomal aberrations as well as their use in biological research has been published over the years (e.g., Coe et al, 1988; Carlson, 1988; Sheridan, 1982; Neuffer et al, 1968). This information is presently being incorporated into the Maize Genome Database that is under development by Ed Coe and colleagues. Any available stock(s) will be sent upon request without charge.

Mutant alleles are useful to maize scientists in many different areas of research. These mutations act as coordinates on genetic or physical maps of the maize genome. In addition, many define critical steps in metabolic, developmental, and other pathways of great interest to geneticists, physiologists, breeders, molecular biologists, chemists and other maize scientists. The materials at the Stock Center are also available to educational institutions for teaching purposes.

While the vast majority of the mutants in the collection are too extreme for commercial use and are not usually evaluated and maintained with a view to their direct use in improving agricultural production or products, some of the mutants in our collection clearly have had a major impact of commercial importance. These include the white endosperm mutants, several of the mutants involved in starch biosynthesis (e.g., su1 and sh2 have been important in sweet corn production, wx1 gives starch high in amylopectin, ae1 gives starch high in amylose), and ig1 for use in making double haploids enabling the rapid production of new inbred lines or placing a desired inbred genotype into a new cytoplasmic background (e.g., male sterile). The other mutants give maize scientists a greater understanding of corn as a biological organism and thus can lead to applications that will improve corn agronomically.

Changes at the Maize Genetics Cooperation * Stock Center since 1992

1) A reel-type irrigation system was obtained that should provide much greater assurance of perpetuating field-grown stocks that are weak or ill-adapted to heat or drought stress conditions.

2) A new low-humidity coldroom has been built, essentially doubling our seed storage capacity. This additional capacity found immediate use for storage of seed samples that were held at room temperature pending availability of supplementary long-term storage. It will also be needed in the near future for stocks anticipated to be received from other established collections. The new coldroom is already currently serving as a repository for newly acquired maize collections. We have obtained stocks from the collections of Marcus Rhoades, George Sprague, Barbara McClintock, and Donald Robertson, and are in the process of obtaining stocks from the collections of Charles Burnham and Walton Galinat. We expect the collection to expand considerably over the next few years to accommodate the collections of maize geneticists retiring from active research.

3) We have purchased two Macintosh computers that are hooked into the Internet. We have started accepting stock requests via e-mail (our internet address is maize@uiuc.edu). We are in the process of entering stock pedigree and availability data into our internal database. This information will make pedigree analysis and planting decisions easier. It is anticipated that computerizing the Stock Center's data will enable us to enhance our service to the maize research community.

4) We have been collaborating with Ed Coe's efforts in creating a Maize Genome database. This is part of the Plant Genome database effort being sponsored by the National Agricultural Library. We have plans to tie our internal database in with MaizeDB (and therefore also with the PGD [Plant Genome Database] at NAL and also with GRIN [Germplasm Resources Information Network] (See article on page 21)) to allow users access to the latest information about available maize genetic stocks. Presently, our list of available stocks is accessible via Gopher and the World Wide Web (WWW) from PGD and MaizeDB (the full Sybase version is also accessible by the public). With the help of Quinn Sinnott, data on available maize genetic stocks has also been entered into GRIN. A list of available stocks will continue to be published annually as part of the Maize Genetics Cooperation * Newsletter.

We anticipate that in addition to current methods for requesting stocks (mail, phone, FAX and e-mail), a user will be able to find a stock of interest in an on-line database and directly request stocks from within the database program. The request will be transmitted electronically through the Internet to us. We hope to have direct ordering available via Gopher, WWW and from the MaizeDB Sybase database soon.

5) Research programs are being established at the Maize Genetics Cooperation * Stock Center. Our goal is to establish a center for Maize Genetics research that will enhance our service to the maize genetics community. For further information, or to send in a seed request, contact us at:

Maize Genetics Cooperation *
Stock Center
S-123 Turner Hall
1102 South Goodwin Avenue
Urbana, IL 61801-4798
(217) 333-6631 [phone]
(217) 333-6064 [fax]
maize@uiuc.edu [Internet]

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◆

Introducing Dr. Olin D. Anderson

Dr. Olin D. Anderson is Supervisory Research Geneticist in the Crop Improvement and Utilization Research Unit, based at the ARS Western Regional Research Center, Albany, California. In this position, which he has held since 1989, he serves as project leader for wheat bioengineering efforts. The project's mission is twofold: to develop the technology for generating wheat with improved agronomic characteristics, such as disease and pest resistance; and to diversify the crop using the improved traits.

Dr. Anderson also serves as Triticeae Database Coordinator and is a member of the Wheat Crop Advisory Council.

He began his USDA career as an Edminster Fellow (1982-84), before joining the Department as a research biologist, a position he held from 1984 to 1988. Since 1988, he has published 20 articles on wheat biology topics.

He became interested in wheat genetics for the "opportunity to improve a crop important not only to the U.S., but to the entire world," adding that wheat is the most widely grown crop in the world, and the most important source of protein in the human diet.

Before joining USDA, Dr. Anderson was a NIH Fellow at the University of California, Berkeley, (1977-81), the same institution from which he graduated with a B.A. in Zoology (1971).

Dr. Anderson received his Ph.D. from Purdue University, West Lafayette, Indiana, in 1977, where he also completed a NIH Predoctoral Fellowship (1971-75) and a David Ross Fellowship (1976).

He is also a member of several professional organizations, including American Association for the Advancement of Science, American Society of Plant Physiologists, International Society of Plant Molecular Biologists, Crop Science Society of America, and American Association of Cereal Chemists. ◆

Competitive Edge

1994 Plant Genome Grant Recipients

G. Adam, K. Kindle
Cornell University
Retrofitting YAC Clones for Plant Transformation

S. Baker
University of Detroit Mercy
A Model System to Assess the Environmental Risks in Releasing Transgenic Plants

A. Bendich
University of Washington
The Structure and Replication of the Plant Mitochondrial Genome

J. Bennetzen
Purdue Research Foundation
Parallel Studies of Genome Microorganization in Maize, Sorghum and Rice

J. Bennetzen
Purdue Research Foundation
Multi-Institutional Research Coordination Group on Integration of Grass Genome Studies

J. Birchler
The Curators of the University of Missouri
Chromosomal Manipulation in Maize

D. Bird
University of California
Molecular Analysis of Nematode-Induced Plant Nurse Cells

A. Bockholt
Texas A&M Research Foundation
Development of Molecular Probes to Augment Breeding for Quality Protein Maize

W. Cande
The Regents of the University of California
Cytological Map of Maize Pachytene Chromosomes

V. Chandler
Gordon Research Center-Gordon Research Conferences
University of Rhode Island
1994 Gordon Conferences on Plant Molecular Biology Regulatory Mechanisms in Plants

V. Chandler
University of Oregon
Allelic Diversity and Tissue Specific Control of the Maize b Regulatory Gene

C. Chase
University of Florida
Selectable Markers for Direct Mictochondrial Transformation in Higher Plants

C. Chen
Board of Regents of the University of Wisconsin
Cytokinin-Regulated Transcription

V. Citovsky
The Research Foundation of State University of New York
Nuclear Import of Nucleic Acid-Protein Complexes in Plants

E. Coe, S. Chao, G. Davis, M. McMullen
Mid-West Area, Agricultural Research Service
U. S. Department of Agriculture
Plant Mutants and Leaf cDNAs Mapped in Concert

M. Cooley
Individual Awardee
Site-Selected Insertional Mutagenesis of the Polygalacturonase Gene of Tomato

D. Crowell
Indiana University
Cytokinin-Regulated mRNA Stability in Soybean Cells

A. Das
The Regents of the University of Minnesota
Transformation of Recalcitrant Plants by an Agrobacterium tumefaciens Mutant

W. Dawson
University of Florida
Plant Resistance and Recognition of Tobamoviruses

J. Deikman
The Pennsylvania State University
Regulation of Gene Expression by Ethylene During Tomato Fruit Ripening

E. del Campillo
Individual Awardee
Function of Multiple Cellulases in Tomato Flower Abscission Zones

S. Dellaporta
Yale University
The Molecular Genetics of Sex Determination in Maize

E. De Rocher
Individual Awardee
Post-Transcriptional Control of ERI Gene Expression by Ethylene in Tomato

C. Deutch
The Board of Regents of the University of Nevada
Structure and Expression of Proline Dehydrogenase Genes

R. Dewey
North Carolina State University
Characterization of the Cholinephosphotransferase Gene of Soybean

R. Doerge
Individual Awardee
Quantitative Trait Mapping: A New Statistical Approach

D. Gallie
The Regents of the University of California
Isolation of RNA-Binding Proteins Involved in Regulating Translation

C. Gasser
The Regents of the University of California, Davis
Genetic Analysis of Ovule Development

R. Gaudino
Individual Awardee
Hormonal and Developmental Regulation of rRNA Transcription in *A. thaliana*

B. Gill, J. Jiang
Kansas State University
Molecular Cytogenetics and Plant Genome Mapping

F. Gmitter, G. Moore
University of Florida
Genome Mapping to Facilitate Disease-Resistant Citrus Cultivar Development

W. Gruissem
Gordon Research Center-Gordon Research Conference
1994 Gordon Conference on Mitochondria and Chloroplasts

W. Gruissem
The Regents of the University of California
Tomato Inositol Monophosphatase - Structure, Function, and Regulation

W. Gurley
University of Florida
Characterization of Transcription Factor IIB in Plants

J. Gustafson, J. Dille
Mid-West Area, Agricultural Research Service
U. S. Department of Agriculture
Molecular Cytogenetics of *Triticum* and *Oryza*: Physical Mapping of RFLP Markers

S. Hake
Federation of American Societies for Experimental Biology
FASEB Summer Research Conference: Plant Development and Cell Biology

A. Handa, R. Joly, J. Gaffe, D. Tieman
Purdue University
Function of Pectin Methylesterase in Plant Growth and Development

L. Hannah
University of Florida
Biochemical Characterization of Maize QTLs

C. Hedgcoth
Kansas State University
Wheat Mitochondrial DNA and Cytoplasmic Male Sterility

A. Huang
The Regents of the University of California, Riverside
Molecular and Cell Biology of Oil Bodies in Seeds

A. Hunt
University of Kentucky Research Foundation
Characterization of a Plant Poly(A) Polymerase

T. Hymowitz, R. Singh
The Board of Trustees of the University of Illinois
Cytogenetics of the Genus Glycine: Broadening the Genetic Base of the Soybean

M. James, A. Myers
Iowa State University of Science and Technology
Characterization of the Maize Gene Sugery1, a Determinant of Starch Composition in Kernels

G. Johal
The Curators of the University of Missouri
Molecular Analysis of Genes Conferring Resistance to Leaf Spot/Ear Rot Disease of Maize

L. Kaufman
University of Illinois at Chicago
Isolation of the Blue Light Receptor and the Blue Light Activated G-Protein

M. Kyle
Cornell University
Genome Mapping and Broad Spectrum Disease Resistance

C. Lamb
Salk Institute for Biological Studies
Gene Activation Mechanisms in the Initiation of Plant Defense Responses

N. Lapitan
Colorado State University
Molecular Tagging and Pyramiding of Russian Wheat Aphid Resistance Genes in Wheat

B. Liu, R. Sederoff
North Carolina State University
Linkage Map Merging Problem

J. Lu
Florida A&M University
Tagging Viticulturally Important Genes by DNA Markers

S. MacKenzie, G. Martin
Purdue Research Foundation
Map-based Cloning of a Plant Gene That Influences the Mitochondrial Genome

M. Maguire
The University of Texas at Austin
Nature and Function of Meiotic Genetic Elements Concerned with Fertility

W. Marcotte
Clemson University
Post-Transcriptional Regulation of the Wheat Em Gene

M. Saghai Maroof, G. Buss, S. Tolin
Virginia Polytechnic Institute and State University
High Resolution Mapping of a Soybean Chromosomal Region Containing Virus Resistance Genes

R. Martienssen
Cold Spring Harbor Laboratory
The Role of the Hcf106 Gene Product in Thylakiod Membrane Biogenesis

S. McCormick
Pacific West Area, Agricultural Research Service
U.S. Department of Agriculture
Positional Cloning of Male Sterile Genes of Tomato

T. McCoy
Montana State University
Studies on Introgression and Inbreeding Alfalfa Using Molecular Markers

L. McIntosh
Michigan State University
Effects of Engineered Plant Respiration on Growth/ Yield and Lowered Temperatures

M. McMullen, P. Byrne, M. Snook, N. Widstrom
Mid-West Area, Agricultural Research Service
U.S. Department of Agriculture
Genetic Control of Corn Earworm Resistance Factors in Maize

J. Medford
The Pennsylvania State University
Schizoid Signal Reception in the Vegetative Shoot Apex

M. Melan
Duquesne University
Isolation and Characterization of *Arabidopsis thaliana* MAP Genome

R. Michelmore, H. Witsenboer
The Regents of the University of California, Davis
Pre-Selected Microsatellite Markers for Lettuce

J. Mullet
Texas A&M Research Foundation
Mapping and Analysis of Genes Controlling Sorghum Maturity

R. Mulligan
The Regents of the University of California
RNA Editing in Plant Mitochondria

M. Mutschler, J. Steffens
Cornell University
Genomic Regions Associated with Multiple Pest Resistance and Acylsugar Biosynthesis

J. Nasrallah, M. Nasrallah
Cornell University
A Structural and Transcriptional Analysis of the S-Locus Region of *Brassica*

N. Nielsen
Mid-West Area, Agricultural Research Service
U.S. Department of Agriculture
Post-Translational Processing and Assembly of Soybean Glycinin

J. Norris
University of Rhode Island
Expression of Modulin Genes and Chalcone Synthase in Mutants of Sweetclover

L. Oberthur
Montana State University
Genomic Differences Associated with Variation in Winter hardiness in Barley

T. Okita
Washington State University
Localization of Prolamine mRNAs to the Protein Body Endoplasmic Reticulum

C. Opperman, M. Conkling
North Carolina State University
Characterization of a Nematode-Responsive Plant Gene Promoter

T. Osborn
The Board of Regents of the University of Wisconsin, Madison
Defining Genes for Vernalization Requirement in *Brassica*

D. Ow
Pacific West Area, Agricultural Research Service
U.S. Department of Agriculture
Recombinase-Based in vivo, and in vitro Manipulation of the Plant Genome

C. Pikaard
Washington University
Genetic Mechanisms Controlling Nucleolar Dominance in *Brassica* Amphidoploids

R. Plaisted, C. Yencho
Cornell University
RFLP Techniques Applied to Insect and Nematode Resistance in Potatoes

G. Presting
Individual Awardee
Characterization and Cloning of a Plant Centromere

T. Quayle
The Board of Regents of the University of Wisconsin, Parkside
Structure/Function of Maize Palindromic DNA Repeat and Associated Binding Proteins

D. Rains, A. Lauchli
University of California
Fifth International Symposium on Genetics and Molecular Biology of Plant Nutrition

W. Rapp
The Curators of the University of Missouri - St. Louis
Transcriptional Regulatory Mechanisms in Plant Mitochondria

T. Reynolds
University of North Carolina
Isolation and Characterization of Elements of the Gram-Negative Bacterial Transposon, Tn1721, in Wheat

E. Richards
Washington University
Genomic Organization of a Plant Centromere

J. Rogers
The Curators of the University of Missouri-Columbia
Hormonal and Endosperm-Specific Regulation of Genes in Barley

P. Ronald, J. Salmeron
The Regents of the University of California, Davis
Molecular Characterization of Tomato Mutants Altered in Pathogen Recognition

D. Samac
Mid-West Area, Agricultural Research Service
U.S. Department of Agriculture
Activation of Defense Response Genes of Alfalfa by the Root-Lesion Nematode

R. Schmidt, M. Yanofsky
The Regents of the University of California, San Diego
An Analysis of Floral Regulatory Genes in Maize

P. Schnable, R. Wise
Iowa State University of Science and Technology
Molecular Characterization of Fertility Restoration in T-Cytoplasm Maize

M. Schuler
The Board of Trustees of the University of Illinois
Plant Cytochrome P450s

W. Sheridan
University of North Dakota
Genetic Regulation of Maize Female Gametophyte Development

N. Sinha
Trustees of Boston University
The ADHERENT Locus in Maize: Genetic and Molecular Analysis of Cell Fusions

M. Sorrells, A. Van Deynze, S. McCouch
Cornell University
Comparative Mapping of *Gramineae* Family

D. Spooner
Mid-West Area, Agricultural Research Service
U. S. Department of Agriculture
Molecular Characterization of the Wild Potato Solanum brevicaule Complex

S. Strauss, W. Adams, F. Sorensen
Oregon State University
Mapping of Genes Related to Adaptation in Douglas-Fir Hybrids

C. Stuber, M. Senior
South Atlantic Area, Agricultural Research Service
U.S. Department of Agriculture
Development of a Simple Sequence Repeat Map in Maize

S. Tanksley
Cornell University
Map-based Cloning of Major Disease Resistance Genes from Tomato

T. Thomas
Texas A&M Research Foundation
Regulation of Plant Embryo Gene Expression

R. Wang, K. Jensen
Northern Plains Area, Agricultural Research Service
Second International *Triticeae* Symposium (Research Conference Support)

R. Whetten, D. Werner
North Carolina State University
Measurement of Somatic Mutation Rate in a Tree

R. Wing
Texas A&M Research Foundation
Development of Map-based Cloning in Crop Plants: Tomato as a Model System

M. Varagona
New Mexico State University
Nuclear Targeting of Anthocyanin Regulatory Proteins

R. Vierstra
The Board of Regents of the University of Wisconsin, Madison
Molecular and Biochemical Analysis of Ubiquitin Conjugating Enzymes in Higher Plants

Z. Yang
Ohio State University Research Foundation
Analyses of the RHO Family of GTP-Binding Proteins from the Garden Pea

N. Young
The Regents of the University of Minnesota
Cloning Plant Genes Known Only by Phenotype-Conference

J. Zeevaart
Michigan State University
Photoperiodic Control of Gibberellin Metabolism in Long-Day Rosette Plants

Z. Zeng, C. Basten, B. Weir
North Carolina State University
Algorithms and Programs for Mapping Quantitative Trait Loci

The FLP Recombinase: A New Tool for Crop Genetics.

Jim Wallis and Dan Guerra
Department of Microbiology, Molecular Biology, and Biochemistry, University of Idaho
Moscow, ID

Early advances in the alteration of plant genomes by application of recombinant DNA technology were not directed to commercial crop varieties. However, many crop plants have now been stably transformed with useful genes and their progeny examined for inheritance of the introduced traits.

Truly successful improvement of crop plants via recombinant DNA technology has been limited both by the methodology of introducting new or altered genes into plants, and by the difficulties of regenerating whole plants after the necessary manipulative steps.

There are other problems associated with using this new technology in crop improvement programs. Current methods of gene transfer all introduce the DNA as random insertions. Such random insertions can result in undesirable changes in phenotype or in a loss of control over the expression of the transgene. In addition, current gene transfer techniques depend on the co-introduction of a selectable antibiotic marker along with the transgenes of interest, which are typically non-selectable. Further problems arise because we have not yet perfected the ability to target new genetic material to a specific locus in the plant genome.

One method of addressing these problems is by use of a site-specific DNA recombinase. Progress has been made using both the cre recombinase, a product of lambda phage in *Escherichia coli*, and the FLP recombinase, an enzyme native to the 2 micron plasmid of *Saccharomyces cerevisiae*.

These recombinases alter the arrangement of DNA sequences in very specific ways. The FLP recombinase is active at a particular 34 base pair DNA sequence, termed the FRT (FLP recombinase target) sequence. When two of these FRT sites are present, the FLP enzyme creates double-stranded breaks in the DNA strands, exchanges the ends of the first FRT with those of the second target sequence, and then reattaches the exchanged strands. This process leads to inversion or deletion of the DNA which lies between the two sites. Whether there is an inversion or deletion depends on the orientation of the FRT sites: if the sites are in the same direction, the intervening DNA will be deleted, but if the sites are in opposite orientation, the DNA is inverted.

Developments

The FLP recombinase is currently being used to genetically engineer crop species. One immediate goal is to use the recombinase to remove antibiotic resistance genes in transgenic plants. Since there is currently public concern over the presence of such antibiotic resistance markers, removal of the resistance gene will improve the marketability of transgenic plant products. Marker removal will also permit use of the original selectable marker to introduce other useful genes into these engineered plants. The FRT site that remains after resistance marker deletion will also provide a means for multiple subsequent insertions of transgenes into a single site in the genome. Introduction of new genes at specific locations may avoid the phenotypic irregularities and problems with expression that result from random integration.

Finally, the FLP recombinase could be used as a negative selectable

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Home Base

Simple Search Tools Can Save Time

Genome Informatics Group
Information Systems Division
USDA, ARS, National Agricultural Library
Beltsville, MD

The Genome Informatics Group at the National Agricultural Library now offers eight plant databases, encompassing *Arabidopsis*, rice, maize, the triticeae, the solanaceae, *Chlamydomonas*, soybeans, and forest trees. While integrating these into one unified environment remains a formidable technical problem, two very simple tools—WAIS[1] and agrep[2]—make it possible to search one or more databases with a single query. Both are available via the ACEDB World Wide Web (WWW) interface at http://probe.nalusda.gov:8300. To use them, your web viewer will need to handle html forms correctly (the current release of NCSA Mosaic does so for all platforms).

WAIS and agrep queries are particularly useful if your search can be expressed as one or a few words or if you want to examine every record (or "*object*") in a database (the information is in there somewhere, but where?). Even if you are interested in only one database, the searches are convenient enough for routine use. In addition, agrep supports "fuzzy" searches, described in more detail below.

Searching with WAIS

WAIS is an indexing and searching system that is familiar to many Gopher users. It can be applied to WWW-based information as well to allow rapid, simple queries. We have used WAIS to index nearly every word in the databases available to us (some words are suppressed because they occur too frequently to be useful). A WAIS search is initiated by opening the WAIS form (the WWW page listing all the databases contains a link to it). Use the check boxes to select the databases you wish to search. By default the search is limited to the plant databases. If your query is successful, you will obtain a list of objects that you can click on in the usual way to obtain additional information. If you have searched more than one database at the same time, the list may contain objects from different databases.

WAIS syntax is easy to master. By default WAIS looks for complete, exact (but case-insensitive) matches. For example, if you search for *photo*, only objects that contain the word *photo* will be returned. An object containing the word *photograph* will not be detected. Partial word matching is provided by adding a wildcard, in this case an asterisk (*), to the end of a word (*e.g., photo**). Thus, if your first search returns nothing, try the same word with an asterisk at the end. You can only use the asterisk to extend a word. For example, **hoto* and *ph*to* will not match *photo*.

If you enter a series of words (*word1 word2 word3*...), the response will be a list of objects that contain matches to at least one of the query words. In this case WAIS is treating the list as if the Boolean operator OR were present as a search modifier (*word1 or word2 or word3*). A search can also use the operators AND and NOT. Literal phrase matching is provided when the phrase is sur-

1. WAIS is copyright (c) MCNC, Clearinghouse for Networked Information Discovery and Retrieval, 1993.
2. Wu and Manber, "Fast Test Searching With Errors," Technical report #91-11, Department of Computer Science, University of Arizona, June 1991.

rounded by either single or double quotes. For example, the query *"light harvesting"* will only return objects that exactly contain that phrase.

Searching with agrep

"Fuzzy" or approximate searches with agrep make it possible to identify objects which do not exactly match your query. This is particularly useful if you are uncertain how to spell an item exactly (was it *adh-1* or *adh1*?). The form for the agrep query is almost identical to that for WAIS, allowing one or more databases to be selected for screening. The response to the query will be a list of objects from one or more databases, depending on which sources you selected.

Type your search pattern into the text box and click the search button to begin the search. By default the search assumes case doesn't matter and that the pattern is surrounded by whitespace. If you are searching more than one database, be patient. Searching every one of the databases (well over 200 MB) might take more than a minute. You can use wildcards, but note that agrep uses # instead of * for this purpose (the asterisk has another meaning to agrep). The Boolean operator AND is represented by a semicolon. Thus *Jones;Smith* will identify any objects containing BOTH of these patterns. OR is represented by a comma. *Jones,Smith* will identify objects containing one or both patterns.

An agrep search is fuzzy if you allow mismatching. Use the radio buttons on the agrep form to set the number of mismatches. For example, massechusets matches massachusetts with two errors (one substitution and one insertion). If you want certain parts of the pattern to match exactly, put that part inside angle brackets (<>). For example, <mathemat>ics matches mathematical with one error (replacing the last s with an a), but mathe<matics> does not match mathematical no matter how many errors or substitutions are allowed.

WAIS and agrep limitations

Although WAIS and agrep both support multi-database queries, it is important to understand that the way data is organized varies considerably across databases. For example, one database may store information about people and organizations in a category called "Person" while another may use "Colleague." Within the categories themselves there are often differences that can have a significant impact on the results that a query returns. Thus queries should not be expected to yield uniform results from one database to the next.

Even though WAIS and agrep queries can include wildcards (or, in the case of agrep, mismatches), neither tool offers a full complement of pattern matching options. However, a more flexible "regular expression" search tool may become available soon.

Finally, many queries are difficult or impossible to express as WAIS or agrep expressions. In these cases another query method may be more appropriate. "Query by example" and the "query builder" are both tools that are part of the ACEDB software. Each database listed on the WWW interface page has a link to these tools, which operate within the context of one database at a time.

Conclusions

NAL's genome databases can be queried using a spectrum of tools which range in complexity from WAIS and agrep through "query by example," the "query builder," and the ACEDB query language itself. While WAIS and agrep are simple tools, they offer the most efficient methods for screening entire databases for words or phrases.

Queries can be the Achilles' heel of any data retrieval system, and the perfect query interface has yet to be demonstrated for any software. It is therefore important to continue development in this area, especially to support users who are interested in more complex cross-species comparisons. ◆

FLP-cont. from page 18

marker for experiments to replace genes by homologous recombination. An antibiotic resistance marker flanked by FRT sites and regions homologous to the crop plant genome would be deleted if a more distant recombinase gene was inserted in the genome by illegitimate recombination; homologous recombinants would not contain the FLP coding sequence and would retain antibiotic resistance.

Genetic manipulation by means of this eukaryotic recombinase will mark a significant advance in the biotechnological improvement of crop plants. ◆

Germplasm Resources Information Network (GRIN)

Database Management Unit of the
National Germplasm Resources Laboratory
Agricultural Research Service
United States Department of Agriculture
Beltsville, MD

GRIN is the database support system for the collection and dissemination of information on the germplasm of plants, animals, insects, microbes and forest trees. These groups comprise the National Genetic Resources Program (NGRP).

One part of the NGRP is the National Plant Germplasm System (NPGS). The NPGS is a cooperative effort between Federal, State, and private industries. It has the following mission: to acquire, preserve, evaluate and distribute genetic resources to users worldwide.

GRIN aids the NPGS by providing a way for both suppliers and users of germplasm to:

- record accessions,
- monitor accessions via inventory information,
- track genetic "shift" of an accession,
- enter evaluations and characteristics, and
- conduct searches, track distributions.

Diversity and Distribution of Information

America's abundant and inexpensive supply of food is based on intensive agriculture, which relies on genetic uniformity. This uniformity, however, increases the potential for crop vulnerability to pests and stresses. In the face of agriculture's changing needs, scientists must have access to genetic diversity that can help bring forth new varieties that resist pests, diseases and environmental stresses.

The GRIN plant database system consists of over 440,000 discrete accessions. This system serves the needs of plant scientists and other agricultural researchers by providing the following types of data:

- taxonomy,
- passport,
- source,
- evaluation,
- inventory,
- cooperator, and
- distribution.

Through this system, scientists are able to locate germplasm of interest and request it from the repository.

pcGRIN

pcGRIN is a software package that provides a way to view individual crop information on a personal computer (PC). The information on these crops comes from the GRIN database.

pcGRIN is designed for both experienced and inexperienced users and accommodates most PCs. It provides a series of menus that offer quick, easy access to information in the GRIN database.

pcGRIN does not require a phone line and modem. The only equipment needed is an MS-DOS based microcomputer with at least 640K of memory and a hard drive with 10 to 60 megabytes of free space. The amount of free space needed depends on the crop(s).

The Internet

GRIN

The GRIN system is represented on the Internet using World Wide Web or Gopher servers.

If you have access to the World Wide Web, our URL (Universal Resource Locator) is: http://www.ars-grin.gov

Our Gopher server can be reached by typing: gopher gopher.ars-grin.gov

In some Gopher lists, we can be found as: GRIN, National Genetic Resources Program, USDA-ARS

pcGRIN

pcGRIN also is available by anonymous FTP on the Internet, and can be downloaded onto your machine by following these steps:

- Connect to our machine: ftp.ars-grin.gov
- When it asks for a login, type: anonymous
- When it asks for your password, type: [your e-mail address]
- Change the directory to: /pub/pcgrin
- Set the transfer mode to binary.
- Then get the file for the crop you are interested in. It is listed as: [crop].exe

LAMP

Eleven Latin American countries plus the United States participated in the evaluation of 15,000 varieties of maize. The data from these evaluations describe the characteristics of the plants grown in their respective regions. Later stages of the project will use these characteristics to help create new high yielding varieties and hybrids.

The first and second stages of results were put on a CD-ROM by the GRIN Database Management Unit (DBMU).

Also included on the CD-ROM is maize data from Agriculture Canada, CIMMYT, and the USDA Agricultural Research Service. With the extra space on the CD-ROM, the DBMU added data of 25 other crops in GRIN that are important in the Americas.

Stage four data will be included in the next version of the CD-ROM and should be available in the spring of 1995.

Further Interest and Questions

If you would like more information on GRIN, pcGRIN, or LAMP, contact:

The GRIN Database Management Unit
USDA, ARS
10300 Baltimore Blvd.
Bldg. 003, Room 407
Beltsville, MD 20705
Phone: (301) 504-5666
Fax: (301) 504-5536
e-mail: grin@ars-grin.gov

◆

On the Horizon

Calendar of Upcoming Genome Events

1995 MEETINGS

February 4-9: **Advances in Gene Technology: Protein Engineering and Structural Biology: Miami Bio/ Technology Winter Symposium, Ft. Lauderdale, FL.** Contact: Miami Bio/Technology Winter Symposia, P.O. Box 016129 (M823), Miami, FL 33101. PHN: (800) 642-4363, FAX: (305) 324-5665, EMAIL: mbws@mednet.med.miami.edu

February 13-15: **Second Rice Genome Meeting.** Contact: Ilkka Havukkala, FAX: 81-298-38-2245, EMAIL: ilkka@staff.or.jp

March 5-9: **XVIII Eucarpia Symposium: Ornamental Plant Improvement, Classical and Molecular Approaches, Tel Aviv, Israel.** Contact: Dan Knassim Ltd., P.O. Box 57005, Tel Aviv, 61570 Israel. PHN: (972) 3-5626470, FAX: (972) 3-5612303.

April 7-12: **Plant Mitochondria: From Gene to Function, Durham, NC.** Contact: Jim Siedow, DCMB-Botany, Box 91000, Duke University, Durham, NC 27708-1000. PHN: (919) 613-8180, FAX: (919) 613-8177, EMAIL: jsiedow@acpub.duke.edu

April 23-27: **3rd International Union of Biochemistry and Molecular Biology Conference: Molecular Recognition, Singapore.** Contact: 3rd IUBMB Conference Coordinator, Ken-Air Destination Management Company, 35 Selegie Rd., 09-19 Parklane Shopping Mall, Singapore 0718. PHN: (65) 336-8857/8, FAX: (65) 336-3613.

May 13-17: **Ninth International Biotechnology Meeting & Exhibition, San Francisco, CA.** Contact: Biotechnology Industry Organization, 1625 K St., NW, Suite 1100, Washington, DC 20006-1604. PHN: (202) 857-0244, FAX: (202) 331-8132 or (202) 857-0237.

May 24-26: **Seventh Annual National Agricultural Biotechnology Council Meeting: Genes for the Future: Discovery, Ownership, Access, Columbia, MO.** Contact: National Agricultural Biotechnology Council, 159 Biotechnology Bldg., Cornell University, Ithaca, NY 14853-2703.

July 4-7: **9th International Rapeseed Congress, Cambridge, England.** Contact: Denis Kimber, 44 Church St., Haslingfield, Cambridge, CB3 7JE, England.

July 14-19: **15th International Conference on Plant Growth Substances, Minneapolis, MN.** Contact: Gary Gardner, Dept. of Horticultural Science, University of Minnesota, 305 Alderman Hall, St. Paul, MN 55108. FAX: (612) 624-3606, EMAIL: ggardner@maroon.tc.umn.edu

July 29-August 2: **American Society of Plant Physiologists Annual Meeting, Charlotte, NC.** Contact: Susan Chambers, Director of Finance and Administration, 15501 Monona Dr., Rockville, MD 20855-2768. PHN: (301) 251-0560 ext. 11, FAX: (301) 279-2996, EMAIL: chambers@access.digex.net

August 6-12: **20th World Congress of the International Union of Forestry Research Organisations, Tampere, Finland.** Contact: Professor Risto Seppala, Finnish Forest Research Institute, IUFRO-95, Secretariat Unioninkatu 40A 00170, Helsinki, Finland.

October 1-4: **Engineering Plants for Commercial Products/ Applications, Lexington, KY.** Contact: International Symposium on Engineering Plants, c/o Conferences and Institutes, 218 Peterson Service BIdg., Lexington, KY 40506-0005. PHN: (606) 257-3929, FAX: (606) 323-1053, EMAIL: monica.stoch@ukwang.uky.edu

1995 WORKSHOPS AND COURSES

March 13-17: **Receptor Binding Techniques, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. PHN: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

June 19-30: **An International Training Program in New Crops: Medicinal and Aromatic Plants, West Lafayette, IN.** Contact: Tom Robertson, Attn: International Training Program in Aromatic and Medicinal Plants, Continuing Education, Purdue University, 1586 Stewart Center, West Lafayette, IN 47907-1586. PHN: (317) 494-7220, FAX: (317) 494-0567.

August 6-11: **10th International Workshop on Plant Membrane Biology, Regensburg, Germany.** Contact: Widmar Tanner, Lehrstuhl für Zellbiologie und Pflanzenphysiologie, Universität Regensburg, Universitätsstrasse 31, 93053 Regensburg, Germany. FAX: 49-943-3352.

August 29-31: **Society for Experimental Biology Annual Meeting, Cambridge, England.** Contact: Society for Experimental Biology, Burlington House, London W1V 0LQ, United Kingdom. PHN: 44 171 439 8732, FAX: 44 171 287 4786.

September 1-3: **ITMI International Public Workshop, Norwich, England.** Contact: International Triticeae Mapping Initiative, Management Office, Genetic Resources Conservation Program, University of California, Davis, CA 95616-8602. PHN: (916) 757-8920, FAX: (916) 757-8755, EMAIL: itmi@ucdavis.edu

Release of SBML1 Soybean Germplasm

The United States Department of Agriculture, Agricultural Research Service, announces the release of the soybean germplasm SBML1.

SBML1 germplasm consists of 146 recombinant inbred lines of soybeans derived from the hybridization of the plant introduction Pl290136 and BARC-2 (Rj4), a near isogenic line derived from the cultivar Clark63. These lines were developed by eight successive generations of inbreeding and approach homozygosity for most traits. Homozygous lines retain genetic stability through increased availability of this germplasm. They also enhance the soybean genome mapping program by permitting researchers at other locations to contribute information on these lines to the publicly available genetic database maintained by the Plant Molecular Biology Laboratory.

These recombinant inbred lines are being released to facilitate the genetic mapping of the soybean genome. They have been characterized for genes controlling bacterial pustule resistance, maturity, seed coat color, root fluorescence, flower color and resistance to nodulation by the chlorosis inducing species *Bradyrhizobium elkanii*. A database of molecular markers (RFLPs and RAPDs) is available, and researchers requesting seeds of the recombinant inbred lines are requested to add their data to this database.

Limited quantities of seeds of SBML1 are available to researchers upon written request to T. E. Devine, Plant Molecular Biology Laboratory, Plant Sciences Institute, USDA, ARS, 10300 Baltimore Blvd., Beltsville, MD 20705. When this germplasm contributes to genome mapping research, it is requested that appropriate recognition be given to its source. Genetic material of this release will be deposited in the National Plant Germplasm System, where it will be available for research purposes. ◆

FYI

Oxford Molecular Acquired Intelligenetics, Inc.

Oxford Molecular Group (OMG), the Oxford, England-based computer-aided molecular design company, has announced its intent to acquire IntelliGenetics, Inc. (Mountain View, CA), one of the world's leading developers of DNA and protein sequence analysis software.

Background on IntelliGenetics

IntelliGenetics was formed to commercialize academic research in bioinformatics and associated database management systems. It is one of the leading developers of DNA and protein sequence analysis software in the world. The company was founded in 1980 by four professors from Stanford University. In May 1986, Amoco bought voting control of IntelliGenetics, and the company became a wholly owned subsidiary of Amoco Technology Corporation (ATC) in 1990.

IntelliGenetics' product range presently includes:

- GeneWorks®
  Apple Macintosh software for DNA and protein sequence analysis
- PC/GENE®
  PC software for DNA and protein sequence analysis
- IntelliGenetics® Suite
  Sun and Digital software for DNA and protein sequence analysis
- BIONET™
  An on-line timesharing system for DNA and protein sequence analysis
- GENESEQ™
  A database of protein and nucleic acid sequences extracted from worldwide patent documents
- MPSRCH™
  Rapid and sensitive database searching software for the MasPar massively parallel computer

New products which will enhance user access to databases and offer new analytical features for IntelliGenetics software are under development.

The agreement will afford Oxford Molecular a significant presence in the United States. The company represents over 50 percent of the world market and is home to the other major market vendors.

Commenting on the acquisition, Dr. Tony Marchington, Chief Executive of Oxford Molecular, said, "This acquisition is a major strategic step for Oxford Molecular. We went public on the London Stock Exchange in part so that we could significantly grow our business in the U.S. as well as enter the Biotechnology arena with a bang. We're aggressively pursuing this vision with this acquisition. What's more, IntelliGenetics will benefit from Oxford Molecular's broadly based strategy to be a major supplier of rational drug design services."

Oxford Molecular — with offices in Springfield, Virginia; Palo Alto and San Diego, California; Erlangen, Germany and Paris, France — was the first spin-off company from Isis Innovation, the intellectual property company of the University of Oxford. The company was founded in 1989 to bring molecular science software from the most respected research laboratories into the commercial arena. Following the acquisition in 1993 of its European competitor, BioStructure, it is one of the largest European-based suppliers specializing in computer-aided molecular drug design software. The company went public on the London Stock Exchange in April 1994.

Oxford Molecular has established a number of strategic relationships with pharmaceutical manufacturers, including Glaxo Group Research, British Bio-technology, Hoechst-Roussel Laboratories, Pfizer and SmithKline Beechman. ◆

RiceGenes - An Information System for Rice Research

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The RiceGenes database came into existence in April 1993, funded by a grant from the USDA Plant Genome Research Program. Housed at Cornell University, the database contains a variety of information related to the rice genome and rice germplasm. It is our hope that the construction and free distribution of the database will provide an information tool that is useful to the international rice research community.

For a number of years, rice DNA probes developed and maintained at Cornell University have been freely distributed to rice researchers around the globe. Not only were these probes used to create the original and the expanded high-density molecular maps at Cornell (McCouch et al., 1988, Causse et al., 1994), but they have also been used in molecular mapping efforts in many other rice-producing countries. The initial focus of the database development effort was to make available all information relating to these maps and markers in order to facilitate their efficient use throughout the world.

Among the data included are detailed descriptions of close to 700 DNA markers, as well as the raw mapping data from the interspecific backcross population that is the basis of the Cornell map. A set of molecular maps developed by other programs using subsets of these markers but based on different mapping populations is in the process of being loaded. In addition, the classical genetic map based on known genes and morphological mutant markers is also available in RiceGenes. Estimates of the molecular weights of RFLP bands detected by over 1200 probe/enzyme combinations have been calculated, and images of parental survey blots have been included for over 250 of the probes. We have recently incorporated an extensive data set which includes the molecular characterization of a large sample of rice germplasm. Approximately 150 diverse rice accessions were surveyed with 150 probes, and the molecular weights and banding patterns that resulted were catalogued. Each accession record includes a list of probe/enzyme combinations and the corresponding molecular weights of the bands they produce. Each molecular allele has a link to all accessions in which it was detected, and each probe/enzyme polymorphism record groups the total set of accessions according to like banding patterns. This allows the user to see all other accessions with a similar profile for a given probe/enzyme, to assess how "rare" a particular band is, and to compare the alleles contained in two different accessions.

We will soon have available a maize/rice comparative map containing over 650 markers and showing homologous regions between these two genomes. Images are already available which show the polymorphisms resulting from select probe/enzyme combinations on barley, rice, oat, wheat and sugar cane. Comparative maps of rice, oat, wheat, barley, maize, sorghum and millet are currently under development using rice as the basis for the comparison of these genomes. These maps will also be available through RiceGenes. Work is underway in collaboration with the Japanese Rice Genome Research Program to produce an integrated map which will significantly increase the level of molecular detail available.

To further add to the molecular data, links are being made to rice sequences deposited in the public sequences databases. Links are also being made to the GRIN system,

providing access to performance records for over 50,000 rice accessions. Both of these links will allow RiceGenes users to seamlessly access information from physically discrete databases via the World Wide Web (described below). Finally, we hope to establish collaborations with groups interested in extending RiceGenes, particularly in terms of pest and pathogen information.

For users who have network connections, RiceGenes is accessible via the Internet in four formats. The first is a graphical user interface based on the ACEDB software which is available to users with direct TCP/IP network connections and X11 graphics capability (this includes most UNIX workstations, or personal computers with some additional, inexpensive software). The ACEDB format provides live graphics, photographic images and text displays, with links between data objects that can be activated by clicking with the mouse. This format is distributed as a compressed .tar file via anonymous ftp from the site probe.nalusda.gov, directory pub/ricegenes. The second format is the gopher, which is menu-driven and has more limited searching powers, but is very easy to use and requires no special graphics capabilities. Duplicate gopher servers are maintained at nightshade.cit.cornell.edu port 70 and probe.nalusda.gov port 7007 to ensure continuous service. Gopher access requires only a modem connection to an Internet host. The third method of access is through the World Wide Web. The USDA/NAL provides access to all plant genome databases, and much more, through a Web server located at the following URL (electronic address): http://probe.nalusda.gov:8000. Depending on the viewer software used, the Web can be a graphical interface (e.g., using Mosaic) or text-only (e.g., using Lynx). In either case, the Web provides the capability of hot links between, in addition to within, databases. The final interface is an electronic mail query system for users who do not have full Internet access, but do have Internet mail service. Send a message to waismail@probe.nalusda.gov with only the word "help" in the body of the message to receive instructions on using this service.

In addition to the full contents of the database (both text and images), the gopher and Web interfaces have access to electronic versions of the Rice Genetics Newsletter. We currently have three volumes of the Newsletter available as text documents which are preindexed for fast searching by any word, and will ultimately include all twelve volumes. The electronic, word-searchable versions of such documents are expected to be more useful to a wider group of people than the printed versions.

For non-Internet sites, the National Agricultural Library has made available a CD-ROM which contains all the USDA-funded genome databases. More information on the CD-ROM and other information services provided by the USDA can be obtained from pgenome@nalusda.gov.

Perhaps to a greater extent than the other USDA genome databases, RiceGenes must address an international user group. Broadly speaking, the goal of the project is to provide an accessible source of information on rice genetic resources, and in particular to provide the type of information that may be costly or impossible for many labs to produce or accumulate by themselves. Researchers around the world are strongly encouraged to participate in the expansion of the database by making their results publicly available through this forum. Because much of the research being done on rice is carried out in countries which do not have access to the Internet, the distribution of the plant genome databases on CD-ROM was strongly lobbied for and has been key in the dissemination of the RiceGenes information.

For further details regarding the database or how to access it please contact: Edie Paul, 252 Emerson, Ithaca, NY 14583, or via electronic mail to epaul@nightshade.cit.cornell.edu.

Literature Cited:

McCouch SR, Kochert G, Yu ZH, Wang ZY, Khush GS, Coffman WR, Tanksley SD (1988) Molecular mapping of rice chromosomes. Theor Appl Genet 76:815-829

Causse M, Fulton TM, Cho YG, Ahn SN, Chunwongse J, Wu K, Xiao J, Yu Z, Ronald PC, Harrington SB, Second GA, McCouch SR, Tanksley SD (1994) Saturated molecular map of the rice genome based on an interspecific backcross population. Genetics (in press). ◆

Plant Genome Publications

The following publications are available. If you would like to receive a copy, check off the title and mail your request to:

Plant Genome Data and Information Center
National Agricultural Library, USDA
10301 Baltimore Blvd., 4th Floor
Beltsville, MD 20705-2351

CRIS/ICAR Projects and Bibliographies:

The sponsored research projects were obtained by searching CRIS/ICAR (USDA and CARC, North America) using AGRISEARCH Silver Platter CD. Bibliographies were obtained by searching AGRICOLA Silver Platter CD.

- **DNA Fingerprinting and Plant.** November 1994. Compiled by Andrew Kalinski.
- **Gene Tagging in Plants.** December 1994. Compiled by Andrew Kalinski.
- **Molecular Markers in Plant Genome Analysis.** December 1994. Compiled by Andrew Kalinski.
- **Transgenic Cotton.** December 1994. Compiled by Andrew Kalinski.
- **Transgenic Wheat.** December 1994. Compiled by Andrew Kalinski.
- **Transposable Elements in Plants.** December 1994. Compiled by Andrew Kalinski.

Miscellaneous Publications:

Prepared by the Biotechnology Information Center staff.

- **AG/Biotechnology Electronic Information.**
- **ALF (Agricultural Library Forum): The National Agricultural Library's Electronic Bulletin Board System -- Brief Guide.** Prepared by Karl Schneider
- **Biotechnology Directories.**
- **Databases Pertaining to Biotechnology.**
- **Guide to Information Sources in Biotechnology.**
- **Newsletters Pertaining to Agricultural Biotechnology.**

Other Informational Products:

Prepared by the Genome Informatics Group.

- **Plant Genome Database CD-ROM**

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